

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	thermogenic protein	USPAT	ADJ	ON	2004/06/08 20:36

***** Welcome to STN International *****

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America

NEWS 2 "ask CAS" for self-help around the clock

NEWS 3 JAN 27 Source of Registration (SR) information in REGISTRY updated and searchable

NEWS 4 JAN 27 A new search aid, the Company Name Thesaurus, available in CA/Caplus

NEWS 5 FEB 05 German (DE) application and patent publication number format changes

NEWS 6 MAR 03 MEDLINE and LMEDELINE reloaded

NEWS 7 MAR 03 MEDLINE file segment of TOXCENTER reloaded

NEWS 8 MAR 03 FRANCEPAT now available on STN

NEWS 9 MAR 29 Pharmaceutical Substances (PS) now available on STN

NEWS 10 MAR 29 WPIFV now available on STN

NEWS 11 MAR 29 New monthly current-awareness alert (SDI) frequency in RAPRA

NEWS 12 APR 26 PROMT: New display field available

NEWS 13 APR 26 IFIPAT/IFIUDS/IFICDB: New super search and display field available

NEWS 14 APR 26 LITALERT now available on STN

NEWS 15 APR 27 NIDS: New search and display fields available

NEWS 16 May 10 PROUSDDR now available on STN

NEWS 17 May 19 PROUSDDR: One FREE connect hour, per account, in both May and June 2004

NEWS 18 May 12 EXTEND option available in structure searching

NEWS 19 May 12 Polymer links for the POLYLINK command completed in REGISTRY

NEWS 20 May 17 FRFILL now available on STN

NEWS 21 May 27 STN User Update to be held June 7 and June 8 at the SIA 2004 Conference

NEWS 22 May 27 New UPN (Update Code Maximum) field for more efficient patent SDIs in Caplus

NEWS 23 May 27 Caplus super roles and document types searchable in REGISTRY

NEWS 24 May 27 Explore APOLLIT with free connect time in June 2004

NEWS EXPRESS MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.00c(JP), AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004

NEWS HOURS STN Operating Hours Plus Help Desk Availability

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***** STN Columbus *****

FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004

=> index biosci

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE ENTRY 0.21

TOTAL SESSION 0.21

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOSUBSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DEGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 20:39:16 ON 08 JUN 2004

70 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0* with SET DETAIL OFF.

=> s (thermogenic (w) protein) (p) (skunk (w) cabbage)

0* FILE ADISNEWS
0* FILE BIOCOMMERCE
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
0* FILE CIN
25 FILES SEARCHED...

0* FILE ESBIODASE

0* FILE FEDRIP
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
1 FILE IFIPAT
0* FILE KOSMET
0* FILE MEDICNF
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
62 FILES SEARCHED...

1 FILES HAVE ONE OR MORE ANSWERS, 70 FILES SEARCHED IN STNINDEX

L1 QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

=> file hits

COST IN U.S. DOLLARS

SINCE FILE ENTRY 1.14

TOTAL SESSION 1.35

FULL ESTIMATED COST

FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004

COPYRIGHT (C) 2004 IFI CLAIMS(R) Patent Services (IFI)

FILE COVERS 1950 TO PATENT PUBLICATION DATE: 3 JUN 2004 (20040603/PD)

FILE LAST UPDATED: 4 JUN 2004 (20040604/ED)

HIGHEST GRANTED PATENT NUMBER: US2004087609

HIGHEST APPLICATION PUBLICATION NUMBER: US2004107471

UNITERM INDEXING IS AVAILABLE IN THE IFIUDS FILE

UNITERM INDEXING LAST UPDATED: 27 MAY 2004 (20040527/UP)

INDEXING CURRENT THROUGH PAT PUB DATE: 25 Nov 2003 (20031125/PD)
IFIPAT has been reloaded (12/21/2003). See HELP RLOAD for details.

=> s 11
64 THERMOGENIC
65668 PROTEIN
37 SKUNK
450 CABBAGE
L2 1 (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

=> d 12 bib ab

L2 ANSWER 1 OF 1 IFIPAT COPYRIGHT 2004 IFI on STN
AN 10560887 IFIPAT;IFIUDB;IFICDB
TI PLANT THERMOGENIC GENES AND PROTEINS
IN Ito: Kikukatsu, Iwate, JP
IN Ito Kikukatsu (JP)
PAF Unassigned
PA Unassigned Or Assigned To Individual (68000)
AG WENDEROFF, LIND & POWACK, L.L.P., 2033 K STREET N. W., SUITE 800,
WASHINGTON, DC, 20006-1021, US
PI US 2004068105 A1 20040408
AI US 2003-671628 20030929
RI WO 2000-723806 20000612 Section 371 PCT Filing UNKNOWN
RLI US 2002-9982 20020123 DIVISION
PRAI JP 1999-167439 19990614
FI US 2004068105 20040408
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 6

8 Figure(s).

FIG. 1 shows the change of the temperature of the spadix in skunk cabbage and that of ambient temperature with a lapse of time.

FIG. 2 shows the results of northern blotting, indicating the expression profile of SfUCPa (A) and SfUCPb (B) in the spadix and leaf of skunk cabbage at room temperature (RT) and during cold treatment (4 degrees C. for 3 days). The lower figures respectively show the results of ethidium bromide staining of non-decomposed rRNA.

FIG. 3 compares the alignment of amino acid sequences of SfUCPa and SfUCPb, together with potato UCP (StUCP), Arabidopsis UCP (AtPUMP) and human UCP. The asterisk (*) attached under the sequences indicate the same amino acid sequence, and the dot (.) indicates the conservative change in all of the sequences. The boldface indicates the same sequence between SfUCPa and SfUCPb. The gap introduced to optimize the sequence alignment is indicated by a dash (-). The alignment was made using a CLUSTAL W program. The characteristic domains of energy transfer proteins typical of mitochondria are surrounded by a square. The shaded bars (I-VI) above the upper sequence show estimated transmembrane domains. FIG. 4 shows a hydrophobic plot of SfUCPa. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are indicated by TM1 to TM6.

FIG. 5 shows a diagrammatic illustration of SfUCPa topology in the mitochondria membrane.

FIG. 6 shows a hydrophobic plot of SfUCPb. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are

indicated by TM1 to TM4 and TM6.
FIG. 7 shows a diagrammatic illustration of SfUCPb topology in the mitochondria membrane.

FIG. 8 shows the results of in vitro translation using respective cDNAs of the genes SfUCPa and SfUCPb as templates. (i) indicates a control, S a sense RNA, and AS an antisense RNA. The asterisk (*) indicates a non-specific product and the empty circle denotes the position of a low molecular translated artificial product synthesized from a small ORF.

AB Th inventions of his application include thermogenic genes named SfUCPa and SfUCPb which are derived from skunk cabbage. cDNA of each gene comprises the base sequence of SEQ ID NO: 1 and 2, respectively. Thermogenic proteins, SfUCPa and SfUCPb, are expressed from genes SfUCPa and SfUCPb, comprises the amino acid sequence of SEQ ID NO: 2 and 4.

=> d his

(FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPP, CROPU, DISSABS, DDFB, DDFU, DGENE, DRUGB, DRUGMONO2, ...' ENTERED AT 20:39:16 ON 08 JUN 2004

SEA (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

0* FILE ADISNEWS
0* FILE BIOCOMMERCE
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
0* FILE CIN
0* FILE ESSIORAGE
0* FILE FEDRIP
0* FILE FOWAD
0* FILE FOREGE
0* FILE PROSTTI
0* FILE FSTA
0* FILE IFIPAT
1 FILE KOSMET
0* FILE MEDICONF
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
0* QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

L1

FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004

L2 1 S L1

=> log Y

COST IN U.S. DOLLARS

SINCE FILE

ENTRY

5.91

FULL ESTIMATED COST

TOTAL

SESSION

7.26

STN INTERNATIONAL LOGOFF AT 20:40:57 ON 08 JUN 2004

OM protein - protein search, using sw model

Run on: May 18, 2004, 11:11:47 ; Search time 48.3433 Seconds
(without alignments)
1566.356 Million cell updates/sec

Title: US-10-009-962-4
Perfect score: 1382
Sequence: 1 MGDHGPRTETSFAGSSRAAF.....VIMFLTLEQVKFFIKEVPN 268

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1382	100.0	268	4 AAB73298	Aab73298 SfUcPa de
2	1344.5	97.3	303	4 AAB73297	Aab73297 SfUcPa de
3	1049	75.9	306	3 AAG41403	Aag41403 Arabidops
4	1031	74.6	305	3 AAG05380	Aag05380 Arabidops
5	1031	74.6	305	3 AAG48337	Aag48337 Arabidops
6	1024.5	74.1	318	3 AAG48300	Aag48300 Arabidops
7	712.5	51.6	212	3 AAG41404	Aag41404 Arabidops
8	597	43.2	403	2 AAW81588	Aaw81588 Protein e
9	595	43.1	308	2 AAW81595	Aaw81595 Mouse unc

10	595	43.1	308	2 AAW88280	Aaw88280 Mouse unc
11	595	43.1	312	2 AAW81587	Aaw81587 Human unc
12	595	43.1	432	2 AAY29835	Aay29835 Mouse unc
13	595	43.1	432	2 AAW85117	Aaw85117 A murine
14	595	43.1	432	3 AAY77453	Aay77453 Murine mi
15	595	43.1	432	4 AAE04750	Aae04750 Mouse unc
16	594	43.0	309	2 AAW69166	Aaw69166 Human res
17	594	43.0	309	2 AAY28351	Aay28351 UCP2 amin
18	594	43.0	309	2 AAY28352	Aay28352 UCP2 amin
19	594	43.0	309	2 AAY31903	Aay31903 Human unc
20	594	43.0	309	3 AAY44292	Aay44292 Human unc
21	594	43.0	309	3 AAY45002	Aay45002 Tularik h
22	594	43.0	309	4 AAY72342	Aay72342 Human unc
23	594	43.0	309	5 AAU98901	Aau98901 Human unc
24	594	43.0	314	4 AAU09077	Aau09077 Human unc
25	593	42.9	308	2 AAY29834	Aay29834 Mouse unc
26	593	42.9	308	2 AAW85116	Aaw85116 A murine
27	593	42.9	308	3 AAV77452	Aav77452 Murine mi
28	593	42.9	308	4 AAE04729	Aae04729 Mouse unc
29	592	42.8	309	2 AAW24000	Aaw24000 Complete
30	592	42.8	309	2 AAW89546	Aaw89546 Full leng
31	592	42.8	309	2 AAY28353	Aay28353 UCP2 amin
32	592	42.8	309	3 AAY44252	Aay44252 Human mit
33	592	42.8	309	3 AAY97998	Aay97998 Human unc
34	592	42.8	309	3 AAB27018	Aab27018 Protein a
35	592	42.8	309	7 ABO14802	Abo14802 Human pro
36	592	42.8	309	7 ADE54389	Ade54389 Rat Prote
37	592	42.8	312	2 AAW83379	Aaw83379 Human unc
38	592	42.8	312	2 AAW68197	Aaw68197 Human unc
39	592	42.8	312	2 AAW85667	Aaw85667 Human UCP
40	592	42.8	312	2 AAW88279	Aaw88279 Human unc
41	592	42.8	312	2 AAY31904	Aay31904 Human unc
42	592	42.8	312	3 AAY54600	Aay54600 Amino aci
43	592	42.8	312	3 AAY44253	Aay44253 Human mit
44	592	42.8	312	4 AAB74296	Aab74296 Human UCP
45	592	42.8	312	4 AAE04298	Aae04298 Human unc

ALIGNMENTS

RESULT 1
AAB73298
ID AAB73298 standard; protein; 268 AA.
XX
AC AAB73298;
XX
DT 29-MAY-2001 (first entry)
XX
XX SfUcPa derived exothermicity relating gene protein #2.
XX SfUcPa derived exothermicity relating gene; diabetes; obesity;
XX exothermic material; low temperature resistant plant.
XX Symplocarpus foetidus.
PN JP2000354489-A.

XX PD 26-DEC-2000.
XX PF 14-JUN-1999; 99JP-00167439.
XX PR 14-JUN-1999; 99JP-00167439.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2001-260368/27.
XX DR N-PSDB; AAF77826.
XX PT Exothermicity relating genes and proteins, useful in the treatment of
XX PT diabetes and obesity.
XX PS Claim 4; Page 10-11; 15pp; Japanese.
XX CC The present sequence is a protein encoded by a Symlocarpus foetidus
XX CC (SfUCPa) derived exothermicity relating gene. The gene is useful for
XX CC preparation of low temperature resistant plants, and in the treatment of
XX CC diabetes and obesity. The encoded protein is useful as exothermic
XX CC materials for industrial use
XX SQ Sequence 268 AA;
Query Match 100.0%; Score 1382; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.5e-138;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGDHGPRTEISFAGSSRAAFACFAELCTIPDITAKVRLQKAVTGDVVALPKYRGML 60
DB 1 MGDHGPRTEISFAGSSRAAFACFAELCTIPDITAKVRLQKAVTGDVVALPKYRGML 60
QY 61 GTVATTAREEGLSALWKGI VPGHLRQCLFGGLRIGLYBFVKSFYVGDNFVGDIPLSKKIL 120
DB 61 GTVATTAREEGLSALWKGI VPGHLRQCLFGGLRIGLYBFVKSFYVGDNFVGDIPLSKKIL 120
QY 121 AGLTTGALAIIVANPTDLVKVRLQSEGLPPGVPRYSALNAYSTIVKKEGLGALWTGL 180
DB 121 AGLTTGALAIIVANPTDLVKVRLQSEGLPPGVPRYSALNAYSTIVKKEGLGALWTGL 180
QY 181 GPNIAARNAIINAELASVDQVKMSRMWGD SAYKSTFDCFIKTKNDGFLAFYKGFIPN 240
DB 181 GPNIAARNAIINAELASVDQVKMSRMWGD SAYKSTFDCFIKTKNDGFLAFYKGFIPN 240
QY 241 FQRLGSWNVIMFTLEQVKKFFIKEVPN 268
DB 241 FQRLGSWNVIMFTLEQVKKFFIKEVPN 268
RESULT 2
AAB73297
ID AAB73297 standard; protein; 303 AA.
XX AC AAB73297;
XX DT 29-MAY-2001 (first entry)

XX DE sfUCPa derived exothermicity relating gene protein #1.
XX XN sfUCPa derived exothermicity relating gene; diabetes; obesity;
XX XN exothermic material; low temperature resistant plant.
XX OS Symlocarpus foetidus.
XX FN JP2000354489-A.
XX PD 26-DEC-2000.
XX PF 14-JUN-1999; 99JP-00167439.
XX PR 14-JUN-1999; 99JP-00167439.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX XN WPI; 2001-260368/27.
XX DR N-PSDB; AAF77825.
XX PT Exothermicity relating genes and proteins, useful in the treatment of
XX PT diabetes and obesity.
XX PS Claim 3; Page 7-8; 15pp; Japanese.
XX CC The present sequence is a protein encoded by a Symlocarpus foetidus
XX CC (SfUCPa) derived exothermicity relating gene. The gene is useful for
XX CC preparation of low temperature resistant plants, and in the treatment of
XX CC diabetes and obesity. The encoded protein is useful as exothermic
XX CC materials for industrial use
XX SQ Sequence 303 AA;
Query Match 97.3%; Score 1344.5; DB 4; Length 303;
Best Local Similarity 88.1%; Pred. No. 9.7e-134;
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DB 1 MGDHGPRTEISFAGSSRAAFACFAELCTIPDITAKVRLQKAVTGDVVALPKYRGML 60
QY 61 GTVATTAREEGLSALWKGI VPGHLRQCLFGGLRIGLYBFVKSFYVGDNFVGDIPLSKKIL 120
DB 61 GTVATTAREEGLSALWKGI VPGHLRQCLFGGLRIGLYBFVKSFYVGDNFVGDIPLSKKIL 120
QY 121 AGLTTGALAIIVANPTDLVKVRLQSEGLPPGVPRYSALNAYSTIVKKEGLGALWTGL 180
DB 121 AGLTTGALAIIVANPTDLVKVRLQSEGLPPGVPRYSALNAYSTIVKKEGLGALWTGL 180
QY 181 GPNIAARNAIINAELASVDQVKQ-----MK 205
DB 181 GPNIAARNAIINAELASVDQVKQ-----MK 205
QY 206 SRMWGDSAYKSTFDCFIKTKNDGFLAFYKGFIPNFGRLGSNNVIMFTLEQVKKFFIKE 265
DB 241 SRMWGDSAYKSTFDCFIKTKNDGFLAFYKGFIPNFGRLGSNNVIMFTLEQVKKFFIKE 300

QY 266 VFN 268
DB 301 VFN 303

Search completed: May 18, 2004, 11:18:52
Job time : 49.3433 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: May 18, 2004, 11:16:57 ; Search time 15.4886 Seconds
(without alignments)
893.286 Million cell updates/sec

Title: US-10-009-962-4
Perfect score: 1382
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/iaa/ECTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	595	43.1	432	2	US-09-172-528-4 Sequence 4, Appli
3	595	43.1	432	3	US-09-318-199-4 Sequence 4, Appli
4	595	43.1	432	3	US-09-503-579-4 Sequence 4, Appli
5	594	43.0	309	4	US-09-743-847-4 Sequence 4, Appli
6	594	43.0	309	4	US-10-001-051B-2 Sequence 2, Appli
7	593	42.9	308	2	US-08-937-466-2 Sequence 2, Appli
8	593	42.9	308	2	US-09-172-528-2 Sequence 2, Appli
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10	593	42.9	308	3	US-09-503-579-2 Sequence 2, Appli
11	592	42.8	309	1	US-08-518-878B-51 Sequence 51, Appli

12 592 42.8 309 2 US-08-807-861A-51
13 592 42.8 309 2 US-08-470-868A-51
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16 592 42.8 309 4 US-09-547-983-51
17 592 42.8 312 3 US-09-142-565-2
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30 498 36.0 303 1 US-08-518-878B-37
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36 496 35.9 275 4 US-09-808-457-4
37 496 35.9 275 4 US-09-423-410-6
38 469 33.9 256 2 US-08-937-466-6
39 469 33.9 256 2 US-09-172-528-6
40 469 33.9 256 3 US-09-318-199-6
41 469 33.9 256 3 US-09-503-579-6
42 415 30.0 291 4 US-09-501-558-2
43 410.5 29.7 290 4 US-09-743-847-2
44 410.5 29.7 335 4 US-09-482-273-118
45 304 22.0 293 4 US-09-501-558-4

Search completed: May 18, 2004, 11:22:17
Job time : 16.4886 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:20:53 ; Search time 36.6095 Seconds
(without alignments)
2037.017 Million cell updates/sec

Title: US-10-009-962-4
Perfect score: 1382
Sequence: 1 MGDGRTSIFAGSSRAAF.....VINELTLEQVKFFIKEYPN 268

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
---------------	-------	----------------	--------	----	-------------

;	TITLE OF INVENTION: Plant Thermogenic Genes and Proteins	
;	FILE REFERENCE: 2003-1386A/WNC/00653	
;	CURRENT APPLICATION NUMBER: US/10/671,628	
;	CURRENT FILING DATE: 2003-09-29	
;	PRIOR APPLICATION NUMBER: 10/009,962	
;	PRIOR FILING DATE: 2002-01-23	
;	PRIOR APPLICATION NUMBER: PCT/JPO/03806	
;	PRIOR FILING DATE: 2000-06-12	
;	PRIOR APPLICATION NUMBER: JP11-167439	
;	PRIOR FILING DATE: 1999-06-14	
;	NUMBER OF SEQ ID NOS: 12	
;	SOFTWARE: Patentin Ver. 2.0	
;	SEQ ID NO 4	
;	LENGTH: 268	
;	TYPE: PRT	
;	ORGANISM: Symplocarpus foetidus	
;	US-10-671-628-4	
;		
Query Match	100.0%; Score 1382; DB 12; Length	
Best Local Similarity	100.0%; Pred. No. 1.1e-136; Index	
Matches	268; Conservative 0; Mismatches 0; Indels	
QY	1	MGDHGFEITEISFAGSSRAAFACFAELCTCTTETAKVRLQLOKKA
Db	1	MGDHGFEITEISFAGSSRAAFACFAELCTCTTETAKVRLQLOKKA
QY	61	GTVATTAREEGLSALMKGIVFGLRHQCLFGGLRIGLYEPVKSFVYV
Db	61	GTVATTAREEGLSALMKGIVFGLRHQCLFGGLRIGLYEPVKSFVYV
QY	121	AGLTTGALAIIVANPTDLVKVRLQSEGLPGVPRRYSGALNAYS
Db	121	AGLTTGALAIIVANPTDLVKVRLQSEGLPGVPRRYSGALNAYS
QY	181	GFNIARNAIINAEELASVDQVKQKRWMGDSAYKSTPDCFIKTL
Db	181	GFNIARNAIINAEELASVDQVKQKRWMGDSAYKSTPDCFIKTL
QY	241	FGLGSGNNVIMFLTLEQVKKFFKEVPN 268
Db	241	FGLGSGNNVIMFLTLEQVKKFFKEVPN 268
RESULT 2		
US-10-671-628-2		
;	sequence 2, Application US/10671628	
;	Publication No. US20040068105A1	
;	GENERAL INFORMATION:	
;	APPLICANT: ITO, Kikukatsu	
;	TITLE OF INVENTION: Plant Thermogenic Genes and Proteins	
;	FILE REFERENCE: 2003-1386A/WNC/00653	
;	CURRENT APPLICATION NUMBER: US/10/671,628	
;	CURRENT FILING DATE: 2003-09-29	
;	PRIOR APPLICATION NUMBER: 10/009,962	
;	PRIOR FILING DATE: 2002-01-23	
;	PRIOR APPLICATION NUMBER: PCT/JPO/03806	
;	PRIOR FILING DATE: 2000-06-12	

; PRIOR APPLICATION NUMBER: JP11-167439
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 303
; ORGANISM: Symplocarpus foetidus
US-10-671-628-2

Query Match 97.3%; Score 1344.5; DB 12; Length 303;
Best Local Similarity 88.1%; Pred. No. 1.1e-132;
Matches 267; Conservative 0; Mismatches 1; Indels 35; Gaps 1;
QY 1 MGDGPRTEISFAGSSPAACFAELCTIPDLTAKVRLQLOKKA VTDVWALPKYRGML 60
DB 1 MGDGPRTEISFAGSSPAACFAELCTIPDLTAKVRLQLOKKA VTDVWALPKYRGML 60
QY 61 GTVATIAAREEGLSALWKGI VPGHLRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120
DB 61 GTVATIAAREEGLSALWKGI VPGHLRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120
QY 121 AGLTTGALAIIVANPTDLVKRLQSEGLPPGVPRYSGALNAYSTIVKKSGLGALWTGL 180
DB 121 AGLTTGALAIIVANPTDLVKRLQSEGLPPGVPRYSGALNAYSTIVKKSGLGALWTGL 180
QY 181 GNTIARNAIINAAELASVDQVKO-----MK 205
DB 181 GNTIARNAIINAAELASVDQVKO-----MK 205
QY 206 SRMGDSAYKSTFDCFIKTLKNDGFLATYKGFIPNFGRLGSWNVIMFLTEQVKKFFIKE 265
DB 241 SRMGDSAYKSTFDCFIKTLKNDGFLATYKGFIPNFGRLGSWNVIMFLTEQVKKFFIKE 300
QY 266 VPN 268
DB 301 VPN 303

Search completed: May 18, 2004, 11:30:31
Job time : 36.6095 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:16:07 ; Search time 13.6112 Seconds
(without alignments)
1893.978 Million cell updates/sec

Title: US-10-009-962-4
Perfect score: 1382
Sequence: 1 MGDGPRTEISFAGSSPAACFAELCTIPDLTAKVRLQLOKKA VTDVWALPKYRGML 268

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
1	1121	81.1	306	2	T07793	uncoupling protein
2	1049	75.9	306	2	T47570	uncoupling protein
3	1040	75.3	306	2	T52024	uncoupling protein
4	592	42.8	312	2	JC5522	uncoupling protein
5	542	39.2	307	2	G01858	uncoupling protein
6	518	37.5	307	2	S34268	uncoupling protein
7	518	37.5	307	2	A26294	uncoupling protein
8	516	37.3	306	2	A31106	mitochondrial unco
9	504.5	36.5	306	2	A32446	uncoupling protein
10	503.5	36.4	288	2	S03603	uncoupling protein
11	423.5	30.6	305	2	H86274	F7A19.22 protein -
12	421.5	30.5	313	2	D84613	hypothetical prote
13	419.5	30.4	313	2	T05577	uncoupling protein

410.5	28.7	343	2	T15253	hypothetical prote
409.5	28.6	325	2	JC7553	brain mitochondria
360.26	30.0	323	2	T25459	hypothetical prote
344.29	30.2	2	T25459	2-oxoglutarate/mal	
338.24.5	30.2	2	S65040	2-oxoglutarate/mal	
334.5	30.2	2	S65042	2-oxoglutarate/mal	
334.5	30.2	314	2	A36305	2-oxoglutarate/mal
331.24.0	29.7	2	T07405	oxoglutarate/malat	
324.5	31.4	2	A56650	2-oxoglutarate car	
317.5	23.0	2	S44091	oxoglutarate/malat	
291.5	21.1	282	2	T49268	probable dicarboxy
275.19.9	29.8	2	S12351	hypothetical prote	
274.5	19.9	320	2	T37603	probable oxaloacet
273.5	19.8	324	2	S25357	mitochondrial unco
272.7	19.5	331	2	T51899	probable 2-oxoglu
266.5	19.3	322	2	S57116	probable carrier p
247.5	17.9	311	2	A46595	tricarboxylate tra
246.5	17.8	415	2	T48171	hypothetical prote
241.5	17.5	312	2	H98567	hypothetical prote
235.5	17.0	309	2	T48156	hypothetical prote
232.5	16.8	301	2	S51132	ADP, ATP carrier p
232.5	16.8	311	2	G01789	citrate transporte
232.5	16.4	373	2	S48451	probable membrane
226.5	16.4	479	2	T493971	peroxisomal Ca-dep
224.5	16.2	702	2	T16533	hypothetical prote
223.5	16.2	298	1	XWBO	ADP ATP carrier pr
223.5	16.2	381	2	T51158	hypothetical prote
221.5	16.0	300	2	T15206	hypothetical prote
217.5	15.7	298	2	S43446	ADP, ATP carrier pr
215.5	15.6	99	2	S16082	uncoupling protein
215.5	15.6	299	2	S44554	citrate transport
212.5	15.4	358	2	T09109	envelope protein L
211.5	15.3	313	2	T23207	hypothetical prote

ALIGNMENTS

uncoupling protein (clone StUCP7), mitochondrial - potato
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07793
C:Author: R.J.Laloi, M.; Klein, M.; Riesmeier, J.W.; Mueller-Roeber, B.; Fleury, C.; Bouillaud, F.; Ricquier, D.
C:Title: A plant cold-induced uncoupling protein.
C:Reference number: 216136, MUID:97441051, PMID:9296489
C:Accession: T07793
C:Status: preliminary; translated from GB/EMBL/DDBJ
C:Molecule type: mRNA
C:Residues: 1-306 <AL>
C:Cross-references: EMBL:Y11220; NID:92398828; PIDN:CAA72107.1; PID:g2398829
C:Experimental source: cv. Desiree
C:Genetics:
C:Genome: nuclear
C:Superfamily: ADP ATP carrier protein; ADP ATP carrier protein repeat homology

OM protein - protein search, using sw model

Run on: May 18, 2004, 11:12:22 ; Search time 9.38704 Seconds
(without alignments)
1486.603 Million cell updates/sec

Title: US-10-009-962-4
Perfect score: 1382
Sequence: 1 MGDHGPRTEISFAGSRAAF.....VIMFTLEQVKFFKEVFN 268

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601	43.5	310	1	UCP2_CYPQA Q9W235 cyprinus ca
2	600.5	43.5	311	1	UCP3_BOVIN O77792 bos taurus
3	597.5	43.2	311	1	UCP3_CANFA Q9N219 canis famli
4	595	43.1	308	1	UCP3_MOUSE P56501 mus musculu
5	595	43.1	309	1	UCP2_MOUSE P70406 mus musculu
6	595	43.1	310	1	UCP2_BRARE Q9W720 brachydanic
7	594	43.0	309	1	UCP2_HUMAN P55851 homo sapien
8	593	42.9	308	1	UCP3_RAT P56499 rattus norv
9	593	42.9	309	1	UCP2_PIG O37562 sus scrofa
10	592	42.8	309	1	UCP2_RAT P56500 rattus norv
11	592	42.8	312	1	UCP3_HUMAN P55916 homo sapien
12	587	42.5	309	1	UCP2_CANFA Q9N2J1 canis famli
13	583	42.2	308	1	UCP3_PIG O37649 sus scrofa
14	541	39.1	307	1	UCP1_HUMAN P25874 homo sapien
15	518	37.5	306	1	UCP1_MESAU P04575 mesocricetu
16	518	37.5	306	1	UCP1_RAT P04633 rattus norv
17	516	37.3	306	1	UCP1_MOUSE P12242 mus musculu

18	509.5	36.9	306	1	UCP1_RABIT
19	503.5	36.4	288	1	UCP1_BOVIN
20	436	31.5	323	1	UCP4_HUMAN
21	410.5	29.7	325	1	UCP5_HUMAN
22	406.5	29.4	325	1	UCP5_MOUSE
23	366	26.5	287	1	DIC_HUMAN
24	351.5	25.4	287	1	DIC_MOUSE
25	334.5	24.2	313	1	M2OM_BOVIN
26	333.5	24.1	313	1	M2OM_MOUSE
27	334.5	23.5	313	1	M2OM_HUMAN
28	318.5	23.0	313	1	M2OM_RAT
29	273.5	19.8	324	1	OAC1_YEAST
30	266.5	19.3	322	1	SFC1_YEAST
31	247.5	17.9	311	1	TXTP_RAT
32	241.5	17.5	312	1	TXTP_CAEEL
33	232.5	16.8	311	1	TXTP_HUMAN
34	231.5	16.8	311	1	TXTP_BOVIN
35	226.5	16.4	373	1	VIA6_YEAST
36	226	16.4	675	1	CMC2_HUMAN
37	224.5	16.2	702	1	CMC1_CAEEL
38	224	16.2	299	1	ODC_HUMAN
39	223.5	16.2	297	1	ADT1_BOVIN
40	222.5	16.1	316	1	MFTC_MOUSE
41	222	16.1	300	1	MCAT_ARATH
42	220	15.9	676	1	CMC2_MOUSE
43	219.5	15.9	678	1	CMC1_HUMAN
44	219	15.8	298	1	ODC_RAT
45	217.5	15.7	298	1	ADT3_BOVIN

Search completed: May 18, 2004, 11:19:24

Job time : 10.387 secs

OM protein - protein search, using sw model

Run on: May 18, 2004, 11:11:47 ; Search time 54.6567 Seconds

(without alignments)
1566.356 Million cell updates/sec

Title: US-10-009-962-2

Perfect score: 1561

Sequence: 1 MGDHGPRTISFAGSSRAAF.....VIMFLTLQVKKFKIKEVEN 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1960s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1561	100.0	303	4	AAB73297
2	1344.5	86.1	268	4	AAB73298
3	1232.5	79.0	306	3	AAG41403
4	1206.5	77.3	305	3	AAG05380
5	1206.5	77.3	305	3	AAG48337
6	1190	76.2	318	3	AAG48300
7	896	57.4	212	3	AAG41404
8	748	47.9	177	3	AAG41405
9	685.5	43.9	308	2	AAW81595

10	685.5	43.9	308	2	AAW88280	AAW88280 Mouse unc
11	685.5	43.9	432	2	AAZ29835	AAZ29835 Mouse unc
12	685.5	43.9	432	2	AAW85117	AAW85117 A murine
13	685.5	43.9	432	3	AAW77453	AAW77453 Murine ml
14	685.5	43.9	432	4	AAE04730	AAE04730 Mouse unc
15	685.5	43.8	308	2	AAZ29834	AAZ29834 Mouse unc
16	683.5	43.8	308	2	AAW85116	AAW85116 A murine
17	683.5	43.8	308	3	AAW77452	AAW77452 Murine ml
18	683.5	43.8	308	4	AAE04729	AAE04729 Mouse unc
19	682.5	43.7	397	2	AAW81596	AAW81596 Protein e
20	680.5	43.6	403	2	AAW81588	AAW81588 Protein e
21	678.5	43.5	312	2	AAW81587	AAW81587 Human res
22	677.5	43.4	309	2	AAW69166	AAW69166 Human res
23	677.5	43.4	309	2	AAZ28352	AAZ28352 UCP2 amin
24	677.5	43.4	309	5	AAU98901	AAU98901 Human unc
25	677.5	43.4	309	7	AAE54389	AAE54389 Rac Prote
26	675.5	43.3	312	2	AAW83379	AAW83379 Human unc
27	675.5	43.3	312	2	AAW68197	AAW68197 Human unc
28	675.5	43.3	312	2	AAW85667	AAW85667 Human UCP
29	675.5	43.3	312	2	AAW88279	AAW88279 Human unc
30	675.5	43.3	312	2	AAW31904	AAW31904 Human aci
31	675.5	43.3	312	3	AAW54600	AAW54600 Amino aci
32	675.5	43.3	312	3	AAW44253	AAW44253 Human mit
33	675.5	43.3	312	4	AAW74296	AAW74296 Human UCP
34	675.5	43.3	312	4	AAE04298	AAE04298 Human unc
35	675.5	43.3	312	4	AAW68050	AAW68050 Amino aci
36	675.5	43.3	312	5	ABB81610	ABB81610 UCP3L pro
37	675.5	43.3	312	5	AAE19348	AAE19348 Human mit
38	675.5	43.3	312	7	AAE54391	AAE54391 Human Pro
39	674.5	43.2	309	2	AAZ28351	AAZ28351 UCP2 amin
40	674.5	43.2	309	2	AAW31903	AAW31903 Human unc
41	674.5	43.2	309	3	AAZ44292	AAZ44292 Human unc
42	674.5	43.2	309	3	AAW45002	AAW45002 Tularik h
43	674.5	43.2	309	4	AAW72342	AAW72342 Human unc
44	674.5	43.2	314	4	AAU09077	AAU09077 Human unc
45	672.5	43.1	309	2	AAW24000	AAW24000 Complete

ALIGNMENTS

RESULT 1

AAB73297

ID AAB73297 standard; protein; 303 AA.

XX AC AAB73297;

XX AC AAB73297;

XX DT 29-MAY-2001 (first entry)

XX DE SFUCA derived exothermicity relating gene protein #1.

XX KW SFUCA derived exothermicity relating gene; diabetes; obesity;

XX KW exothermic material; low temperature resistant plant.

XX OS Symplocarpus foetidus.

XX PN JP2000354489-A.

XX PD 26-DEC-2000.

XX XX

PF 14-JUN-1999; 99JP-00167439.
XX PR 14-JUN-1999; 99JP-00167439.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2001-260368/27.
XX DR N-PSDB; AAF77825.
XX Exothermicity relating genes and proteins, useful in the treatment of
XX diabetes and obesity.
XX Claim 3; Page 7-8; 15pp; Japanese.
XX The present sequence is a protein encoded by a Symplocarpus foetidus
XX (SFUCPa) derived exothermicity relating gene. The gene is useful for
XX preparation of low temperature resistant plants, and in the treatment of
XX diabetes and obesity. The encoded protein is useful as exothermic
XX materials for industrial use
XX SQ Sequence 303 AA;
Query Match 100.0%; Score 1561; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.5e-151;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLDTAKVRLQLOKKAVTGDVVALPKYRGM 60
DB 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLDTAKVRLQLOKKAVTGDVVALPKYRGM 60
QY 61 GTVATTIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120
DB 61 GTVATTIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120
QY 121 AGLTTCALAIIVANPTDLVKVRLQSEGLPPGVPRYSGALNAYSTIVKKEGLGALWTGL 180
DB 121 AGLTTCALAIIVANPTDLVKVRLQSEGLPPGVPRYSGALNAYSTIVKKEGLGALWTGL 180
QY 181 GPNIAENAIINAAELASYDVQVKOTILKLPFSDNIFTHILAGLGAGFFAVCIGSPVDVWK 240
DB 181 GPNIAENAIINAAELASYDVQVKOTILKLPFSDNIFTHILAGLGAGFFAVCIGSPVDVWK 240
QY 241 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRI GSNVIMFLTLEQVKKFFIKE 300
DB 241 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRI GSNVIMFLTLEQVKKFFIKE 300
QY 301 VEN 303
DB 301 VEN 303
RESULT 2
AAB73298
ID AAB73298 standard; protein; 268 AA.
XX AC AAB73298;
XX

DT 29-MAY-2001 (first entry)
XX SFUCPa derived exothermicity relating gene protein #2.
XX KW SFUCPa derived exothermicity relating gene; diabetes; obesity;
XX KW exothermic material; low temperature resistant plant.
XX OS Symplocarpus foetidus.
XX JF20000354489-A.
XX PD 26-DEC-2000.
XX PF 14-JUN-1999; 99JP-00167439.
XX PR 14-JUN-1999; 99JP-00167439.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2001-260368/27.
XX DR N-PSDB; AAF77826.
XX Exothermicity relating genes and proteins, useful in the treatment of
XX diabetes and obesity.
XX Claim 4; Page 10-11; 15pp; Japanese.
XX The present sequence is a protein encoded by a Symplocarpus foetidus
XX (SFUCPa) derived exothermicity relating gene. The gene is useful for
XX preparation of low temperature resistant plants, and in the treatment of
XX diabetes and obesity. The encoded protein is useful as exothermic
XX materials for industrial use
XX SQ Sequence 268 AA;
Query Match 86.1%; Score 1344.5; DB 4; Length 268;
Best Local Similarity 88.1%; Pred. No. 7.8e-129;
Matches 267; Conservative 0; Mismatches 1; Indels 35; Gaps 1;
QY 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLDTAKVRLQLOKKAVTGDVVALPKYRGM 60
DB 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLDTAKVRLQLOKKAVTGDVVALPKYRGM 60
QY 61 GTVATTIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120
DB 61 GTVATTIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120
QY 121 AGLTTCALAIIVANPTDLVKVRLQSEGLPPGVPRYSGALNAYSTIVKKEGLGALWTGL 180
DB 121 AGLTTCALAIIVANPTDLVKVRLQSEGLPPGVPRYSGALNAYSTIVKKEGLGALWTGL 180
QY 181 GPNIAENAIINAAELASYDVQVKOTILKLPFSDNIFTHILAGLGAGFFAVCIGSPVDVWK 240
DB 181 GPNIAENAIINAAELASYDVQVKOTILKLPFSDNIFTHILAGLGAGFFAVCIGSPVDVWK 240
QY 241 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRI GSNVIMFLTLEQVKKFFIKE 300
DB 241 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRI GSNVIMFLTLEQVKKFFIKE 300

Db 206 SRMGDSAYKTFDCFIKTLKNDGFLAFYKGFIPNFGRLGSMNVIMFTLEQVKKFFIKE 265
QY 301 VFN 303
|||
Db 266 VFN 268
Search completed: May 18, 2004, 11:18:51
Job time : 56.6567 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:16:57 ; Search time 17.5114 Seconds
(without alignments)
893.286 Million cell updates/sec

Title: US-10-009-962-2
Perfect score: 1561
Sequence: 1 MGDHGRTEISFAGSSRAAF.....VINFLTLEQVKKFFIKEVFN 303

Scoring table: BLOSUM62

Gapcp 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match Length DB				ID	Description
	Score	%	Match	Length		
1	685.5	43.9	432	2	US-08-937-466-4	Sequence 4, Appli
2	685.5	43.9	432	2	US-09-172-528-4	Sequence 4, Appli
3	685.5	43.9	432	3	US-09-318-199-4	Sequence 4, Appli
4	685.5	43.9	432	3	US-09-503-579-4	Sequence 2, Appli
5	683.5	43.8	308	2	US-08-937-466-2	Sequence 2, Appli
6	683.5	43.8	308	2	US-09-172-528-2	Sequence 2, Appli
7	683.5	43.8	308	3	US-09-318-199-2	Sequence 2, Appli
8	683.5	43.8	308	3	US-09-503-579-2	Sequence 2, Appli
9	677.5	43.4	309	4	US-10-001-051B-2	Sequence 2, Appli
10	675.5	43.3	312	3	US-09-142-565-2	Sequence 2, Appli
11	675.5	43.3	312	4	US-09-808-457-2	Sequence 2, Appli

12 675.5 43.3 312 4 US-09-423-410-4 Sequence 4, Appli
13 674.5 43.2 309 4 US-09-743-847-4 Sequence 4, Appli
14 672.5 43.1 309 1 US-08-518-878B-51 Sequence 51, Appli
15 672.5 43.1 309 2 US-08-807-861A-51 Sequence 51, Appli
16 672.5 43.1 309 2 US-08-470-868A-51 Sequence 51, Appli
17 672.5 43.1 309 3 US-09-210-681-51 Sequence 51, Appli
18 672.5 43.1 309 3 US-08-946-719A-51 Sequence 51, Appli
19 672.5 43.1 309 4 US-09-547-983-51 Sequence 51, Appli
20 671.5 43.0 299 1 US-08-518-878B-56 Sequence 56, Appli
21 671.5 43.0 299 2 US-08-470-868A-56 Sequence 56, Appli
22 655.5 42.0 310 4 US-09-743-847-5 Sequence 5, Appli
23 614.5 39.4 307 4 US-09-743-847-3 Sequence 3, Appli
24 605 38.8 306 5 FCT-US94-09799-1 Sequence 1, Appli
25 589.5 37.8 307 2 US-08-807-861A-56 Sequence 56, Appli
26 589.5 37.8 307 3 US-09-210-681-56 Sequence 56, Appli
27 589.5 37.8 307 3 US-08-946-719A-56 Sequence 56, Appli
28 589.5 37.8 307 4 US-09-547-983-56 Sequence 4, Appli
29 579.5 37.1 275 4 US-09-808-457-4 Sequence 6, Appli
30 579.5 37.1 275 4 US-09-423-410-6 Sequence 36, Appli
31 569.5 36.5 303 1 US-08-294-522B-36 Sequence 37, Appli
32 566.5 36.3 303 2 US-08-518-878B-37 Sequence 37, Appli
33 566.5 36.3 303 2 US-08-807-861A-37 Sequence 37, Appli
34 566.5 36.3 303 2 US-08-470-868A-37 Sequence 37, Appli
35 566.5 36.3 303 3 US-09-210-681-37 Sequence 37, Appli
36 566.5 36.3 303 4 US-08-946-719A-37 Sequence 37, Appli
37 566.5 36.3 303 4 US-09-547-983-37 Sequence 37, Appli
38 546.5 35.0 256 2 US-08-937-466-6 Sequence 6, Appli
39 546.5 35.0 256 2 US-09-172-528-6 Sequence 6, Appli
40 546.5 35.0 256 3 US-09-318-199-6 Sequence 6, Appli
41 546.5 35.0 256 3 US-09-503-579-6 Sequence 2, Appli
42 489.5 31.4 291 4 US-09-501-558-2 Sequence 2, Appli
43 481 30.8 290 4 US-09-743-847-2 Sequence 118, App
44 481 30.8 335 4 US-09-482-273-118 Sequence 4, Appli
45 362.5 23.2 293 4 US-09-501-558-4

Search completed: May 18, 2004, 11:22:16
Job time : 18.5114 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:20:53 ; Search time 41.3905 Seconds
(without alignments)
2037.017 Million cell updates/sec

Title: US-10-009-962-2

Perfect score: 1561

Sequence: 1 MGDGRTFISFAGSSRAAF.....VINFTLEQVKFFKEVFN 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/FCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1 1561 100.0 303 12 US-10-671-628-2 Sequence 2, Appli
2 1344.5 86.1 268 12 US-10-671-628-4 Sequence 4, Appli
3 1300.5 83.3 305 12 US-10-424-599-237696 Sequence 237696,
4 1294.5 82.9 306 12 US-10-671-628-5 Sequence 5, Appli
5 1254 80.3 345 12 US-10-425-114-66317 Sequence 6317, A
6 1182.5 75.8 314 12 US-10-671-628-6 Sequence 6, Appli
7 677.5 43.4 309 9 US-09-884-814-8 Sequence 8, Appli
8 677.5 43.4 309 13 US-10-001-051B-2 Sequence 2, Appli
9 677.5 43.4 309 15 US-10-197-019-3 Sequence 3, Appli
10 675.5 43.3 312 9 US-09-734-134-2 Sequence 2, Appli
11 675.5 43.3 312 9 US-09-826-507-2 Sequence 2, Appli
12 675.5 43.3 312 9 US-09-808-457-2 Sequence 2, Appli
13 675.5 43.3 312 12 US-10-671-628-9 Sequence 9, Appli
14 674.5 43.2 309 9 US-09-884-814-1 Sequence 1, Appli
15 674.5 43.2 309 12 US-10-336-472-132 Sequence 132, App
16 674.5 43.2 309 12 US-10-671-628-8 Sequence 8, Appli
17 674.5 43.2 309 14 US-10-270-861-34 Sequence 34, Appli
18 674.5 43.2 309 14 US-10-265-689-1 Sequence 1, Appli
19 674.5 43.2 314 10 US-09-823-886A-4 Sequence 4, Appli
20 672.5 43.1 167 12 US-10-424-599-207728 Sequence 207728,
21 672.5 43.1 309 9 US-09-884-814-6 Sequence 6, Appli
22 670.5 43.0 300 14 US-10-270-861-35 Sequence 35, Appli
23 666.5 42.7 321 12 US-10-336-472-130 Sequence 130, App
24 614.5 39.4 307 10 US-09-823-886A-2 Sequence 2, Appli
25 614.5 39.4 307 12 US-10-037-417-87 Sequence 87, Appli
26 613.5 39.3 307 12 US-10-037-417-88 Sequence 88, Appli
27 613.5 39.3 307 12 US-10-671-628-7 Sequence 7, Appli
28 613.5 39.3 307 14 US-10-270-861-33 Sequence 33, Appli
29 597 37.6 192 12 US-10-424-599-249918 Sequence 249918,
30 583.5 37.4 307 12 US-10-037-417-91 Sequence 91, Appli
31 579.5 37.1 275 9 US-09-808-457-4 Sequence 4, Appli
32 579.5 37.1 284 10 US-09-823-886A-6 Sequence 6, Appli
33 579 37.1 306 12 US-10-037-417-89 Sequence 89, Appli
34 579 37.1 306 12 US-10-037-417-90 Sequence 90, Appli
35 541.5 34.7 271 12 US-10-037-417-26 Sequence 26, Appli
36 539.5 34.6 300 12 US-10-424-599-217619 Sequence 217619,
37 529 33.9 317 12 US-10-424-599-276094 Sequence 276094,
38 524.5 33.6 323 10 US-09-946-374-406 Sequence 406, App
39 524.5 33.6 323 12 US-10-063-745-126 Sequence 126, App
40 524.5 33.6 323 12 US-10-063-512-126 Sequence 126, App
41 524.5 33.6 323 12 US-10-063-513-126 Sequence 126, App
42 524.5 33.6 323 12 US-10-063-515-126 Sequence 126, App
43 524.5 33.6 323 12 US-10-063-549-126 Sequence 126, App
44 524.5 33.6 323 12 US-10-063-569-126 Sequence 126, App
45 524.5 33.6 323 12 US-10-063-551-126 Sequence 126, App

ALIGNMENTS

RESULT 1
US-10-671-628-2
; Sequence 2, Application US/10671628
; Publication No. US20040068105A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Kikukatsu
; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins
; FILE REFERENCE: 2003-1386A/WMC/00653
; CURRENT APPLICATION NUMBER: US/10/671,628

; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 10/009,962
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: PCT/JP00/03806
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: JP11-167439
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Symlocarpus foetidus
US-10-671-628-2

Query Match 100.0%; Score 1561; DB 12; Length 303;
Best Local Similarity 100.0%; Pred. No. 2.4e-150;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLDTKAVRLQKKAATGVDVVALPKYRGL 60
|||||
Db 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLDTKAVRLQKKAATGVDVVALPKYRGL 60
|||||

QY 61 GTVATIAEEGLSALWKGI VFGLRHQCIFGGLRIGLYEPKSFYVGNFVGDIPLSKKIL 120
|||||
Db 61 GTVATIAEEGLSALWKGI VFGLRHQCIFGGLRIGLYEPKSFYVGNFVGDIPLSKKIL 120
|||||

QY 121 AGLTTCALAIIVANPTDLVKVRLQSEGLPPGVPRRYSGALNAYSTIVKKEGLGALMTGL 180
|||||
Db 121 AGLTTCALAIIVANPTDLVKVRLQSEGLPPGVPRRYSGALNAYSTIVKKEGLGALMTGL 180
|||||

QY 181 GPNRIARNAINAAELASYDQVKQTILKLPFGSDNIFTHILAGLGAGFAVCIGSPVDYMK 240
|||||
Db 181 GPNRIARNAINAAELASYDQVKQTILKLPFGSDNIFTHILAGLGAGFAVCIGSPVDYMK 240
|||||

QY 241 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSNNVIMFLTEQYKFFIKE 300
|||||
Db 241 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSNNVIMFLTEQYKFFIKE 300
|||||

QY 301 VPEN 303
|||
Db 301 VPEN 303

RESULT 2
US-10-671-628-4
; Sequence 4, Application US/10671628
; Publication No. US20040068105A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Kikukatsu
; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins
; FILE REFERENCE: 2003-1386A/WMC/00653
; CURRENT APPLICATION NUMBER: US/10/671,628
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 10/009,962
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: PCT/JP00/03806

; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: JP11-167439
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Symplocarpus foetidus
US-10-671-628-4

Query Match 86.1%; Score 1344.5; DB 12; Length 268;
Best Local Similarity 88.1%; Pred. No. 2.3e-128;
Matches 267; Conservative 0; Mismatches 1; Indels 35; Gaps 1;

QY 1 MGDHGPRTEISFAGSSRAAFACFAELCTIPLDTAKVRLQKKAATCDVVVALPKYRGM 60
DB 1 MGDHGPRTEISFAGSSRAAFACFAELCTIPLDTAKVRLQKKAATCDVVVALPKYRGM 60

QY 61 GTVATIAREEGLSALWKGIIVPGLHROCLFGLRIGLIEPYKSFYVGDNFVGDIPLSKKIL 120
DB 61 GTVATIAREEGLSALWKGIIVPGLHROCLFGLRIGLIEPYKSFYVGDNFVGDIPLSKKIL 120

QY 121 AGLTTGALAIIVANPTDLVKVRLQSEKLPVGPVPRYSGALNAYSTIVKKEGLGALWTGL 180
DB 121 AGLTTGALAIIVANPTDLVKVRLQSEKLPVGPVPRYSGALNAYSTIVKKEGLGALWTGL 180

QY 181 GPNIARNAIINAAELASYDQVKQ-----MK 205
DB 181 GPNIARNAIINAAELASYDQVKQ-----MK 205

QY 241 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSWNVIMFLTLBOVKKFFIKE 300
DB 206 SRMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSWNVIMFLTLBOVKKFFIKE 265

QY 301 VPN 303
DB 266 VPN 268

Search completed: May 18, 2004, 11:30:31
Job time : 42.3905 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:16:07 ; Search time 15.3888 Seconds
(without alignments)
1893.978 Million cell updates/sec

Title: US-10-009-962-2
Perfect score: 1561
Sequence: 1 MGDHGPRTEISFAGSSRAAF.....VIMFLTLBOVKKFFIKEVPN 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1294.5	82.9	306	2 T07793	uncoupling protein
2	1232.5	79.0	306	2 T47570	uncoupling protein
3	1232.5	78.4	306	2 T52024	uncoupling protein
4	675.5	43.3	312	2 JC5522	uncoupling protein
5	614.5	39.4	307	2 G01858	uncoupling protein
6	591.5	37.9	307	2 A26294	uncoupling protein
7	589.5	37.8	306	2 A31106	mitochondrial unco
8	583.5	37.4	307	2 S34268	uncoupling protein
9	579	37.1	306	2 A32446	uncoupling protein
10	574	36.8	288	2 S03603	uncoupling protein
11	520	33.3	313	2 D84613	hypothetical prote
12	510	32.7	313	2 T05577	uncoupling protein
13	508	32.5	305	2 H86274	F7A19.22 protein -

[illegible]

ALIGNMENTS

T07793 uncoupling protein (clone StUCP7), mitochondrial - potato
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07793
R:Lalot, M.; Klein, M.; Riesmeier, J.W.; Mueller-Roeber, B.; Fleury, C.; Bouillaud, F.; Ricquier, D.
Nature 389, 135-136, 1997
A:Title: A plant cold-induced uncoupling protein.
A:Reference number: Z16136; MUID:97441051; PMID:9296489
A:Accession: T07793
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-306 <LAL>
A:Cross-references: EMBL:Y11220; NID:G2398828; PIDN:CAA72107.1; PID:G2398829
A:Experimental source: cv. Desiree
C:Genetics:
A:Gene: nuclear
C:Superfamily: ADP/ATP carrier protein
C:Keywords: mitochondrion
A:ADP/ATP carrier protein repeat homology

OM protein - protein search, using sw model

Run on: May 18, 2004, 11:12:22 ; Search time 10.613 Seconds
(without alignments)
1466.603 Million cell updates/sec

Title: US-10-009-962-2
Perfect score: 1561
Sequence: 1 MGDHGPRTSIFAGSRAAF.....VIMFLTLQVKKFFKEVPN 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	685.5	43.9	308	1 UCP3_MOUSE	P56501 mus musculus
2	684	43.8	311	1 UCP3_BOVIN	O77792 bos taurus
3	684	43.8	311	1 UCP3_CANFA	O9n219 canis famil
4	681.5	43.7	308	1 UCP3_RAT	P56499 rattus norv
5	681.5	43.7	309	1 UCP2_PIG	O97562 sus scrofa
6	680.5	43.6	309	1 UCP2_MOUSE	P70406 mus musculus
7	679.5	43.5	310	1 UCP2_CYPFA	O9w725 cyprinus ca
8	677.5	43.4	309	1 UCP2_RAT	P56500 rattus norv
9	675.5	43.3	312	1 UCP3_HUMAN	P55916 homo sapien
10	674.5	43.2	309	1 UCP2_HUMAN	P55851 homo sapien
11	673.5	43.1	310	1 UCP2_BRARE	O9w720 brachydanio
12	669.5	42.9	308	1 UCP3_PIG	O97649 sus scrofa
13	667.5	42.8	309	1 UCP2_CANFA	O9n2j1 canis famil
14	613.5	39.3	307	1 UCP1_HUMAN	P25874 homo sapien
15	591.5	37.9	306	1 UCP1_RAT	P04633 rattus norv
16	589.5	37.8	306	1 UCP1_MOUSE	P12242 mus musculus
17	583.5	37.4	306	1 UCP1_MSAU	P04575 mesocricetu
18	579	37.1	306	1 UCP1_RABIT	P14271 oryctolagus

19	574	36.8	288	1	UCP1_BOVIN	P10861 bos taurus
20	524.5	33.6	323	1	UCP4_HUMAN	O95847 homo sapien
21	481	30.8	325	1	UCP5_MOUSE	O95258 homo sapien
22	478	30.6	325	1	UCP5_MOUSE	O92b22 mus musculus
23	447.5	28.7	287	1	DIC_MOUSE	Q8ubx3 homo sapien
24	430	27.5	287	1	DIC_MOUSE	Q8qxd8 mus musculus
25	420	26.9	313	1	M2OM_MOUSE	P22292 bos taurus
26	419	26.8	313	1	M2OM_MOUSE	Q9cr62 mus musculus
27	409	26.2	313	1	M2OM_HUMAN	Q02978 homo sapien
28	400	25.6	313	1	M2OM_RAT	P97700 rattus norv
29	319	20.4	324	1	OAC1_YEAST	P32332 saccharomyc
30	302	19.3	322	1	SFC1_YEAST	P33303 saccharomyc
31	273	17.5	312	1	TXTP_CABEL	P34519 caenorhabdi
32	272.5	17.5	298	1	ODC_RAT	Q99jd3 rattus norv
33	265.5	17.0	300	1	MCAT_ARATH	Q83xm7 arabidopsis
34	264	16.9	316	1	MFIC_MOUSE	Q8bm98 mus musculus
35	263.5	16.9	299	1	ODC_HUMAN	Q8bqt8 homo sapien
36	263.5	16.9	675	1	CMC2_HUMAN	Q8uj60 homo sapien
37	258.5	16.6	315	1	MFIC_HUMAN	Q8h2d1 homo sapien
38	257.5	16.5	676	1	CMC2_MOUSE	Q9gxx4 mus musculus
39	257	16.5	311	1	TXTP_HUMAN	P33007 homo sapien
40	257	16.5	311	1	TXTP_RAT	P32089 rattus norv
41	256.5	16.4	315	1	MFIC_MACFA	Q95j75 macaca fasc
42	253	16.2	299	1	TXTP_YEAST	P38152 saccharomyc
43	253	16.2	311	1	TXTP_BOVIN	P79110 bos taurus
44	252	16.1	678	1	CMC1_HUMAN	O75746 homo sapien
45	251	16.1	373	1	YIA6_YEAST	P40556 saccharomyc

Search completed: May 18, 2004, 11:19:23
Job time : 11.613 secs

OM protein - protein search, using sw model

Run on: May 18, 2004, 11:15:32 ; Search time 38.2067 Seconds
(without alignments)
2502.235 Million cell updates/sec

Title: US-10-009-962-2
Perfect score: 1561
Sequence: 1 MGDHPRTEISFAGSSRAAF.....VIMPLTLEQVKFFIKEVFN 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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1	1561	100.0	303	10	Q9MBE7	Q9mbc7 symplocarpu
2	1389	89.0	304	10	Q8LNZ1	Q8lnz1 helicodicer
3	1344.5	86.1	268	10	Q9MBE6	Q9mbc6 symplocarpu
4	1294.5	82.9	306	10	Q24391	Q24391 solarium tub
5	1290.5	82.7	306	10	Q8SA58	Q8sa58 lycopersico
6	1261	80.8	310	10	Q854C4	Q854c4 tea mayas (m
7	1232.5	79.0	306	10	Q81845	Q81845 arabidopsis
8	1223.5	78.4	306	10	Q65623	Q65623 arabidopsis
9	1209.5	77.5	300	10	Q9AVG1	Q9avg1 oryza sativ
10	1206.5	77.3	305	10	Q9ZWG1	Q9zwg1 arabidopsis
11	1121	71.8	242	10	Q94FU6	Q94fu6 mangifera i
12	1112	71.2	241	10	Q8W1A4	Q8w1a4 glycine max
13	1092	70.0	241	10	Q8W1A3	Q8w1a3 glycine max
14	1091.5	69.9	286	10	Q9FXQ5	Q9fxq5 triticum ae
15	1083.5	69.4	286	10	Q9FXQ6	Q9fxq6 triticum ae
16	1077.5	69.0	293	10	Q9AVG2	Q9avg2 oryza sativ
17	698.5	44.7	304	13	Q98T90	Q98t90 eupetomena
18	681.5	43.7	307	13	Q90X50	Q90x50 meleagris g
19	681.5	43.7	307	13	Q90X50	Q90x50 meleagris g
20	680.5	43.6	309	11	Q9R246	Q9r246 mus musculu
21	680.5	43.6	309	11	Q8CBU0	Q8cbu0 mus musculu
22	679.5	43.5	309	11	Q9ER17	Q9er17 phodopus su
23	678.5	43.5	307	13	Q9DDT7	Q9ddt7 gallus gall
24	678.5	43.5	309	13	Q7ZVP4	Q7zvp4 brachydanio
25	678.5	43.5	310	6	Q7YRF3	Q7yrf3 antechinus
26	676.5	43.3	299	11	Q9ER16	Q9er16 phodopus su
27	675.5	43.3	307	13	Q8AYM4	Q8aym4 gallus gall
28	657.5	42.1	307	13	Q7ZXX1	Q7zxx1 xenopus lae
29	620	39.7	309	6	Q9GMZ1	Q9gmz1 canis fami
30	618	39.6	273	6	Q9XSE1	Q9xse1 bos taurus
31	615.5	39.4	274	6	Q7YRF2	Q7yrf2 sminthopsis
32	590.5	37.8	307	11	Q9ER18	Q9er18 phodopus su
33	583.5	37.4	307	11	Q8K404	Q8k404 dicrostonyx
34	542	34.7	315	13	Q7T3F5	Q7t3f5 brachydanio
35	530.5	34.0	322	11	Q9EPH7	Q9eph7 rattus norv
36	530.5	34.0	322	11	Q9D6D0	Q9d6d0 mus musculu
37	529.5	33.9	224	13	Q8QG96	Q8qg96 pagrus majo
38	520	33.3	313	10	Q8LDF6	Q8ldf6 arabidopsis
39	520	33.3	313	10	Q8SUY5	Q8sly5 arabidopsis
40	511	32.7	313	10	Q94K32	Q94k32 arabidopsis
41	510	32.7	313	10	Q9SB52	Q9sb52 arabidopsis
42	508	32.5	305	10	Q9X174	Q9x174 arabidopsis
43	505.5	32.4	176	10	Q84SE5	Q84se5 oryza sativ
44	503.5	32.3	340	5	Q9VX14	Q9vx14 drosophila
45	499	32.0	365	11	Q9EPH5	Q9eph5 rattus norv

ALIGNMENTS

RESULT 1					
Q9MBE7					
ID	Q9MBE7	PRELIMINARY;	PRT;	303	AA.
AC	Q9MBE7;				
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	STUCPa.				
GN	STUCPA.				

OS Symplocarpus renifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
OX NCB1_taxid=90003;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
RT "Isolation of two distinct cold-inducible cDNAs encoding plant
RT uncoupling proteins from the spadix of skunk cabbage (Symplocarpus
RT foetidus).";
RL Plant Sci. 149:167-173(1999).
CC -|- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB024733; BAA92172.1; .
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006839; P:mitochondrial transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR02030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 303 AA; 32637 MW; F156B1CB6EC3BBB3 CRC64;

Query Match 100.0%; Score 1561; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 3.4e-126;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLOTAKVRLQLOKAVTGDVVALPKYRGML 60
|||
DB 1 MGDHGPTEISFAGSSRAAFACFAELCTIPLOTAKVRLQLOKAVTGDVVALPKYRGML 60
|||

QY 61 GTVATIAREEGLSALWKGI VPGLEHQCLFQGLRIGLYEPVKSFYVGDNFVGDIFLSKKIL 120
|||
DB 61 GTVATIAREEGLSALWKGI VPGLEHQCLFQGLRIGLYEPVKSFYVGDNFVGDIFLSKKIL 120
|||

QY 121 AGLTGTGALAIIVANFTDLVKVRLQSECKLPQGYPRYSALNAYSTIVKKEGLCALWTGL 180
|||
DB 121 AGLTGTGALAIIVANFTDLVKVRLQSECKLPQGYPRYSALNAYSTIVKKEGLCALWTGL 180
|||

QY 181 GPNIARNAIINAAELASYDQVQTILKLPGFSNIFTHILAGLGAGFFAVCGISFVDVMK 240
|||
DB 181 GPNIARNAIINAAELASYDQVQTILKLPGFSNIFTHILAGLGAGFFAVCGISFVDVMK 240
|||

QY 241 SRMKGDSAYKSTFDCFKTLKNDGLLAFYKGFIPNFGRLGSNNYIMFLTLEQVKKFFIKE 300
|||
DB 241 SRMKGDSAYKSTFDCFKTLKNDGLLAFYKGFIPNFGRLGSNNYIMFLTLEQVKKFFIKE 300
|||

QY 301 VPN 303
|||
DB 301 VPN 303
|||

Search completed: May 18, 2004, 11:20:49
Job time : 40.2067 secs